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TECH CENTER 1600/2900



1600

RAW SEQUENCE LISTING

DATE: 02/12/2003

PATENT APPLICATION: US/09/711,896A

TIME: 10:55:25

Input Set : N:\EBONY'S\EP.txt

Output Set: N:\CRF4\02112003\I711896A.raw

3 <110> APPLICANT: KAYANO, Tohru
 4 TANIGUCHI, Mutsuko
 5 YAMAUCHI, Hiroshi
 6 KURIMOTO, Masashi
 8 <120> TITLE OF INVENTION: Antibody specific to interleukin 18 precursor
 10 <130> FILE REFERENCE: KAYANO=1
 12 <140> CURRENT APPLICATION NUMBER: 09/711,896A
 13 <141> CURRENT FILING DATE: 2000-11-15
 15 <150> PRIOR APPLICATION NUMBER: JP 324,860/99
 16 <151> PRIOR FILING DATE: 1999-11-16
 18 <160> NUMBER OF SEQ ID NOS: 15
 20 <170> SOFTWARE: PatentIn version 3.2
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 36
 24 <212> TYPE: PRT
 25 <213> ORGANISM: Homo sapiens
 27 <400> SEQUENCE: 1
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 30 1 5 10 15
 33 Lys Phe Ile Asp Asn Thr Leu Tyr Phe Ile Ala Glu Asp Asp Glu Asn
 34 20 25 30
 37 Leu Glu Ser Asp
 38 35
 41 <210> SEQ ID NO: 2
 42 <211> LENGTH: 35
 43 <212> TYPE: PRT
 44 <213> ORGANISM: Mus musculus
 46 <400> SEQUENCE: 2
 48 Met Ala Ala Met Ser Glu Asp Ser Cys Val Asn Phe Lys Glu Met Met
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 52 Phe Ile Asp Asn Thr Leu Tyr Phe Ile Pro Glu Glu Asn Gly Asp Leu
 53 20 25 30
 56 Glu Ser Asp
 57 35
 60 <210> SEQ ID NO: 3
 61 <211> LENGTH: 157
 62 <212> TYPE: PRT
 63 <213> ORGANISM: Homo sapiens
 66 <220> FEATURE:
 67 <221> NAME/KEY: MISC_FEATURE
 68 <222> LOCATION: (73)..(73)
 69 <223> OTHER INFORMATION: Xaa is Ile or Thr
 71 <400> SEQUENCE: 3

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73 Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile Arg Asn Leu Asn
74 1 5 10 15
77 Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg Pro Leu Phe Glu Asp
78 20 25 30
81 Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro Arg Thr Ile Phe Ile
82 35 40 45
85 Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly Met Ala Val Thr Ile
86 50 55 60
W--> 89 Ser Val Lys Cys Glu Lys Ile Ser Xaa Leu Ser Cys Glu Asn Lys Ile
90 65 70 75 80
93 Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile Lys Asp Thr Lys
94 85 90 95
97 Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asn Lys
98 100 105 110
101 Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr Phe Leu Ala Cys Glu
102 115 120 125
105 Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys Lys Glu Asp Glu Leu
106 130 135 140
109 Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn Glu Asp
110 145 150 155
113 <210> SEQ ID NO: 4
114 <211> LENGTH: 193
115 <212> TYPE: PRT
116 <213> ORGANISM: Homo sapiens
119 <220> FEATURE:
120 <221> NAME/KEY: PROPEP
121 <222> LOCATION: (1)..(36)
123 <220> FEATURE:
124 <221> NAME/KEY: CHAIN
125 <222> LOCATION: (1)..(157)
127 <220> FEATURE:
128 <221> NAME/KEY: MISC_FEATURE
129 <222> LOCATION: (109)..(109)
130 <223> OTHER INFORMATION: Xaa is Ile or Thr
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134 Met Ala Ala Glu Pro Val Glu Asp Asn Cys Ile Asn Phe Val Ala Met
135 1 5 10 15
138 Lys Phe Ile Asp Asn Thr Leu Tyr Phe Ile Ala Glu Asp Asp Glu Asn
139 20 25 30
142 Leu Glu Ser Asp Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile
143 35 40 45
146 Arg Asn Leu Asn Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg Pro
147 50 55 60
150 Leu Phe Glu Asp Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro Arg
151 65 70 75 80
154 Thr Ile Phe Ile Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly Met
155 85 90 95
W--> 158 Ala Val Thr Ile Ser Val Lys Cys Glu Lys Ile Ser Xaa Leu Ser Cys
159 100 105 110

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162 Glu Asn Lys Ile Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile
163      115      120      125
166 Lys Asp Thr Lys Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly
167      130      135      140
170 His Asp Asn Lys Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr Phe
171 145      150      155      160
174 Leu Ala Cys Glu Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys Lys
175      165      170      175
178 Glu Asp Glu Leu Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn Glu
179      180      185      190
182 Asp
186 <210> SEQ ID NO: 5
187 <211> LENGTH: 157
188 <212> TYPE: PRT
189 <213> ORGANISM: Mus musculus
192 <220> FEATURE:
193 <221> NAME/KEY: MISC_FEATURE
194 <222> LOCATION: (70)..(70)
195 <223> OTHER INFORMATION: Xaa is Met or Thr
197 <400> SEQUENCE: 5
199 Asn Phe Gly Arg Leu His Cys Thr Thr Ala Val Ile Arg Asn Ile Asn
200 1      5      10      15
203 Asp Gln Val Leu Phe Val Asp Lys Arg Gln Pro Val Phe Glu Asp Met
204      20      25      30
207 Thr Asp Ile Asp Gln Ser Ala Ser Glu Pro Gln Thr Arg Leu Ile Ile
208      35      40      45
211 Tyr Met Tyr Lys Asp Ser Glu Val Arg Gly Leu Ala Val Thr Leu Ser
212 50      55      60
W--> 215 Val Lys Asp Ser Lys Xaa Ser Thr Leu Ser Cys Lys Asn Lys Ile Ile
216 65      70      75      80
219 Ser Phe Glu Glu Met Asp Pro Pro Glu Asn Ile Asp Asp Ile Gln Ser
220      85      90      95
223 Asp Leu Ile Phe Phe Gln Lys Arg Val Pro Gly His Asn Lys Met Glu
224      100      105      110
227 Phe Glu Ser Ser Leu Tyr Glu Gly His Phe Leu Ala Cys Gln Lys Glu
228      115      120      125
231 Asp Asp Ala Phe Lys Leu Ile Leu Lys Lys Lys Asp Glu Asn Gly Asp
232      130      135      140
235 Lys Ser Val Met Phe Thr Leu Thr Asn Leu His Gln Ser
236 145      150      155
239 <210> SEQ ID NO: 6
240 <211> LENGTH: 192
241 <212> TYPE: PRT
242 <213> ORGANISM: Mus musculus
245 <220> FEATURE:
246 <221> NAME/KEY: PROPEP
247 <222> LOCATION: (1)..(35)
249 <220> FEATURE:
250 <221> NAME/KEY: CHAIN

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Input Set : N:\EBONY'S\EP.txt

Output Set: N:\CRF4\02112003\I711896A.raw

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251 <222> LOCATION: (1)..(157)
253 <220> FEATURE:
254 <221> NAME/KEY: MISC_FEATURE
255 <222> LOCATION: (105)..(105)
256 <223> OTHER INFORMATION: Xaa is Met or Thr
258 <400> SEQUENCE: 6
260 Met Ala Ala Met Ser Glu Asp Ser Cys Val Asn Phe Lys Glu Met Met
261 1 5 10 15
264 Phe Ile Asp Asn Thr Leu Tyr Phe Ile Pro Glu Glu Asn Gly Asp Leu
265 20 25 30
268 Glu Ser Asp Asn Phe Gly Arg Leu His Cys Thr Thr Ala Val Ile Arg
269 35 40 45
272 Asn Ile Asn Asp Gln Val Leu Phe Val Asp Lys Arg Gln Pro Val Phe
273 50 55 60
276 Glu Asp Met Thr Asp Ile Asp Gln Ser Ala Ser Glu Pro Gln Thr Arg
277 65 70 75 80
280 Leu Ile Ile Tyr Met Tyr Lys Asp Ser Glu Val Arg Gly Leu Ala Val
281 85 90 95
W--> 284 Thr Leu Ser Val Lys Asp Ser Lys Xaa Ser Thr Leu Ser Cys Lys Asn
285 100 105 110
288 Lys Ile Ile Ser Phe Glu Glu Met Asp Pro Pro Glu Asn Ile Asp Asp
289 115 120 125
292 Ile Gln Ser Asp Leu Ile Phe Phe Gln Lys Arg Val Pro Gly His Asn
293 130 135 140
296 Lys Met Glu Phe Glu Ser Ser Leu Tyr Glu Gly His Phe Leu Ala Cys
297 145 150 155 160
300 Gln Lys Glu Asp Asp Ala Phe Lys Leu Ile Leu Lys Lys Lys Asp Glu
301 165 170 175
304 Asn Gly Asp Lys Ser Val Met Phe Thr Leu Thr Asn Leu His Gln Ser
305 180 185 190
308 <210> SEQ ID NO: 7
309 <211> LENGTH: 582
310 <212> TYPE: DNA
311 <213> ORGANISM: Homo sapiens
314 <220> FEATURE:
315 <221> NAME/KEY: CDS
316 <222> LOCATION: (1)..(579)
318 <220> FEATURE:
319 <221> NAME/KEY: misc_feature
320 <222> LOCATION: (73)..(73)
321 <223> OTHER INFORMATION: Xaa is Ile or Thr
323 <220> FEATURE:
324 <221> NAME/KEY: mat_peptide
325 <222> LOCATION: (109)..(579)
327 <400> SEQUENCE: 7
328 atg gct gct gaa cca gta gaa gac aat tgc atc aac ttt gtg gca atg 48
329 Met Ala Ala Glu Pro Val Glu Asp Asn Cys Ile Asn Phe Val Ala Met
330 -35 -30 -25
332 aaa ttt att gac aat acg ctt tac ttt ata gct gaa gat gat gaa aac 96

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Input Set : N:\EBONY'S\EP.txt

Output Set: N:\CRF4\02112003\I711896A.raw

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333 Lys Phe Ile Asp Asn Thr Leu Tyr Phe Ile Ala Glu Asp Asp Glu Asn
334 -20 -15 -10 -5
336 ctg gaa tca gat tac ttt ggc aag ctt gaa tct aaa tta tca gtc ata 144
337 Leu Glu Ser Asp Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile
338 -1 1 5 10
340 aga aat ttg aat gac caa gtt ctc ttc att gac caa gga aat cgg cct 192
341 Arg Asn Leu Asn Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg Pro
342 15 20 25
344 cta ttt gaa gat atg act gat tct gac tgt aga gat aat gca ccc cgg 240
345 Leu Phe Glu Asp Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro Arg
346 30 35 40
348 acc ata ttt att ata agt atg tat aaa gat agc cag cct aga ggt atg 288
349 Thr Ile Phe Ile Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly Met
350 45 50 55 60
352 gct gta act atc tct gtg aag tgt gag aaa att tca ayt ctc tcc tgt 336
W--> 353 Ala Val Thr Ile Ser Val Lys Cys Glu Lys Ile Ser Xaa Leu Ser Cys
354 65 70 75
356 gag aac aaa att att tcc ttt aag gaa atg aat cct cct gat aac atc 384
357 Glu Asn Lys Ile Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile
358 80 85 90
360 aag gat aca aaa agt gac atc ata ttc ttt cag aga agt gtc cca gga 432
361 Lys Asp Thr Lys Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly
362 95 100 105
364 cat gat aat aag atg caa ttt gaa tct tca tca tac gaa gga tac ttt 480
365 His Asp Asn Lys Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr Phe
366 110 115 120
368 cta gct tgt gaa aaa gag aga gac ctt ttt aaa ctc att ttg aaa aaa 528
369 Leu Ala Cys Glu Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys Lys
370 125 130 135 140
372 gag gat gaa ttg ggg gat aga tct ata atg ttc act gtt caa aac gaa 576
373 Glu Asp Glu Leu Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn Glu
374 145 150 155
376 gac tag 582
377 Asp
381 <210> SEQ ID NO: 8
382 <211> LENGTH: 193
383 <212> TYPE: PRT
384 <213> ORGANISM: Homo sapiens
386 <220> FEATURE:
387 <221> NAME/KEY: misc_feature
388 <222> LOCATION: (73)..(73)
389 <223> OTHER INFORMATION: The 'Xaa' at location 73 stands for Thr, or Ile.
391 <400> SEQUENCE: 8
393 Met Ala Ala Glu Pro Val Glu Asp Asn Cys Ile Asn Phe Val Ala Met
394 -35 -30 -25
397 Lys Phe Ile Asp Asn Thr Leu Tyr Phe Ile Ala Glu Asp Asp Glu Asn
398 -20 -15 -10 -5
401 Leu Glu Ser Asp Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile
402 -1 1 5 10

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/711,896A

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; Xaa Pos. 73
Seq#:4; Xaa Pos. 109
Seq#:5; Xaa Pos. 70
Seq#:6; Xaa Pos. 105
Seq#:7; Xaa Pos. 73
Seq#:8; Xaa Pos. 73
Seq#:14; Xaa Pos. 70
Seq#:15; Xaa Pos. 70

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:9,10,11,12,13